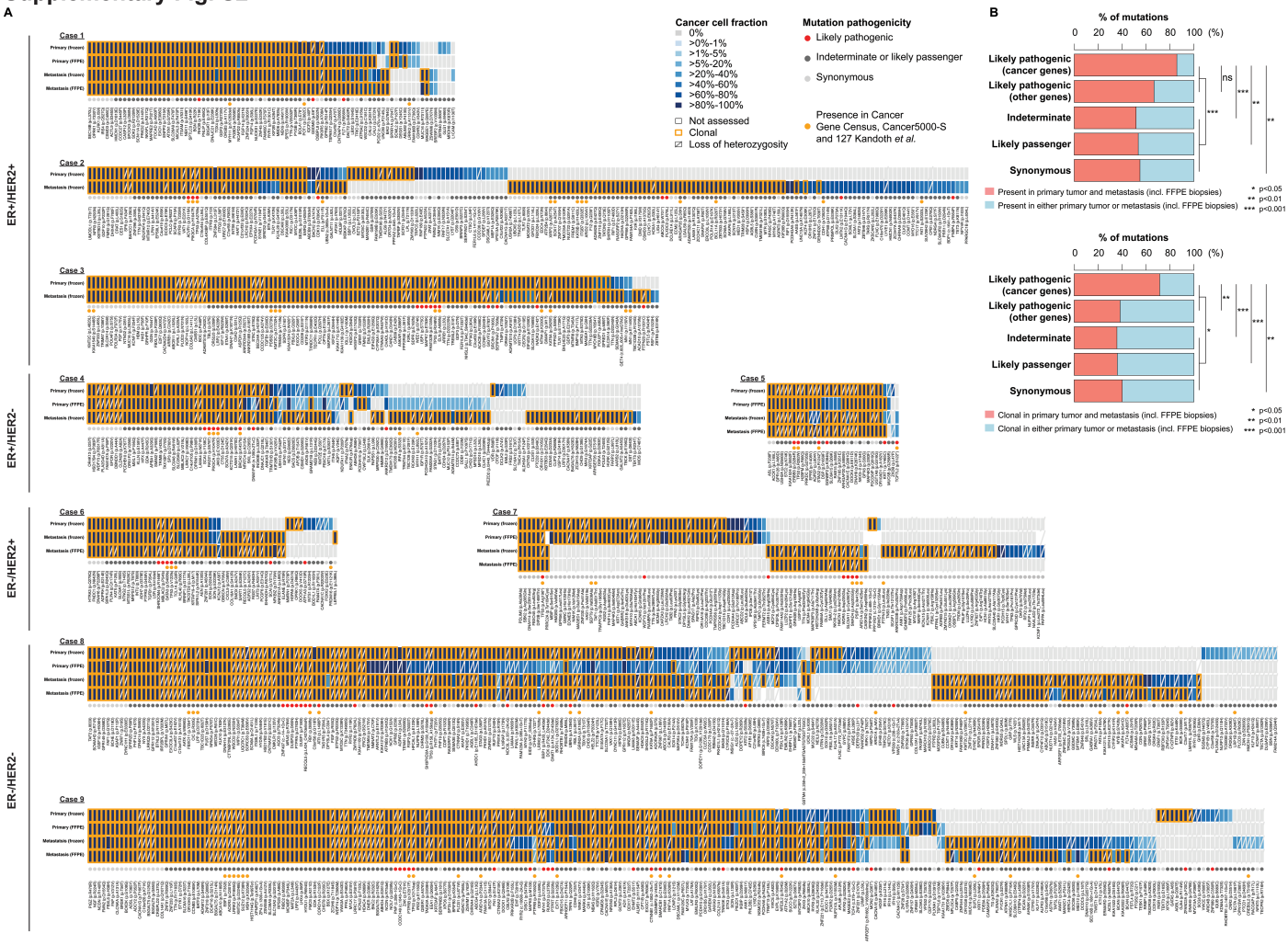
Supplementary Fig. S2



Supplementary Fig. S2: Repertoire of somatic mutations found in the biopsies of primary breast cancers and their metastatic lesions in the nine treatment-naïve patients with *de novo* synchronous metastatic breast cancer. (A) Heatmaps indicate the cancer cell fraction of somatic mutations as determined by ABSOLUTE (24) (blue, see color key) or their absence (grey) in each biopsy (frozen and FFPE where available). Clonal mutations are highlighted in orange boxes and mutations associated with the loss of the wild-type allele are indicated with a diagonal bar. Red, dark grey and light grey dots beneath the heatmap indicate the mutation pathogenicity according to the color key. Mutations affecting cancer genes (31-33) are indicated by orange dots. Cases are grouped according to their ER and HER2 status. **(B)** Barplots of the distribution of mutations (top) present and (bottom) clonal in the frozen and FFPE diagnostic biopsies of the paired primary tumors and the metastatic lesions, classified as likely pathogenic (cancer genes), likely pathogenic (other genes), of indeterminate pathogenicity, likely passenger and synonymous mutations from all patients. Comparisons between the groups of mutations of different pathogenicity were performed using Fisher's exact tests. *: $p < 0.05$, **: $p < 0.01$, ***: $p < 0.001$, ns: not significant.